VL D I Q M T Q T T S S L S A S L G D R V T gatatccagatgacccagactacatcctcctgtctgcctctctgggagacagagtcacc I S C R A S Q D I S N Y L N W Y Q Q K P attagttgcagggcaagtcaggacattagcaattattaaactggtatcagcagaaacca D G T V K L L I Y Y T S I L H S G V P S gatggaactgttaaactcctgatctactacacatcaatattacactcaggagtcccatca R F S G S G S G T D Y S L T I S N L E Q aggttcagtggcagtgggtctggaacagattattctccaccattagcaacctggagcaa E D F A T Y F C Q Q G N T L P W T F G G gaagattttgccacttacttttgccaacaggttaatacgcttccgtggacgttcggtgga G T K L E I K ggcaccaagctggaaatcaaa

VH

E V Q L V E S G G G L V K P G G S L K L gaagtgcagetggtggagtetgggggaggettagtgaagcetggagggteectgaaacte S C A A S G F A F S I Y D M S W V R Q T teetgtgeagcetetggattegetteestateatgatettgggttegecagaet P E K R L E W V A Y I S S G G G T T Y Y ceggagaagaggetggagtggtegeatacattagtagtggtggtggtgcaccetactat P D T V K G R F T I S R D N A K N T L Y ecagacactgtgaagggeegatteaccatetecagagacaatgccaagaacaccetgtac L Q M S S L K S E D T A M Y Y C A R H S etgcaaatgagagactetgaagtetgaggacacagccatgtattactgtgcaagacatagt G Y G S S Y G V L F A Y W G Q G T L V T decagacactgtag

FIG. 1

Nucleotide/residue numbering shown first followed by Kabat Numbering

1	0	49	42 gga GLY G		
2	1 gat ASP D	50	43 act THR T	85	78 ctg LEU L
3	2 atc ILE I	51	44 gtt VAL V	86	79 gag GLU E
4	3 cag GLN Q	52	45 aaa LYS K	87	80 caa GLN Q
5	4 atg MBT M		46 ctc LEU L	88	81 gaa GLU E
6	5 acc THR T	53	40 CCC DEC D		82 gat ASP D
7	6 cag GLN Q	- 54	47 ctg LEU L	89 90	83 ttt PHE F
8	7 act THR T	55	48 atc ILE I		
9	8 aca THR T	56	49 tac TYR Y	91 92	84 gcc ALA A 85 act THR T
10	9 tcc SER S	57	50 tac TYR Y		
11	10 tcc SER S	58	51 aca THR T	93	86 tac TYR Y 87 ttt PHE P
12	11 ctg LEU L	5 9 6 0	52 tca SER S	94	
13	12 tot SER S	60	53 ata ILE I	95 96	88 tgc CYS C 89 caa GLN Q
14	13 gcc ALA A	61	54 tta LEU L	-	90 cag GLN Q
15	14 tet SER S	62·	55 cac HIS H	97 98	91 ggt GLY G
16	15 ctg LEU L	63	56 tca SER S		92 aat ASN N
		64	57 gga GLY G	99	93 acg THR T
		65	58 gtc VAL V	100	94 ctt LEU L
17	16 gga GLY G	66	59 cca PRO P	101	95 ccg PRO P
18	17 gac ASP D	67	60 tca SER S	102	
19	18 aga ARG R	68	61 agg ARG R	103	95A
20	19 gtc VAL V	69	62 ttc PHE F	104	95C
21	20 acc THR T	70	63 agt SER S	105	95D
22	21 att ILE I	71	64 ggc GLY G	106 [.]	95E
23	22 agt SER S	72	65 agt SER S	107	95F
24	23 tgc CYS C	73	66 ggg GLY G	108	
25	24 agj ARG R	74	67 tot SER S	109	97 acg THR T
26	25 gca ALA A	13	68 gga GLY G 69 aca THR T	110	98 ttc PHE F
27	26 agt SER S	76		111	99 ggt GLY G
28	27 cag GLN Q	77	70 gat ASP D 71 tat TYR Y	112 113	100 gga GLY G
29	27A	7 8	72 tot SER S		101 ggc GLY G
30	27B	79	73 ctc LEU L	114 115	101 ggc GHI G
31	27C	80	74 acc THR T		102 acc Ink I
32	27D	81	75 att ILE I	116	103 day bis k
33	27B	62	76 age SER S	117	104 CCG LEC L
34	27F	83	77 aac ASN N	118	105 gaa Gho h
35	28 gac ASP D	84	// dac Aba a	119	106 acc 100 1
36	29 att ILB I			120	107 aaa LYS K
37	30 agc SER S			121	
38	31 aat ASN N			122	108 109 •
39	32 tat TYR Y			123	TA3 -
40	33 tta LEU L		•		
41	34 aac ASN N				
42	35 tgg TRP W				
43	36 tat TYR Y				
44	37 cag GLN Q				
45	38 cag GLN Q				
46	39 aaa LYS K				

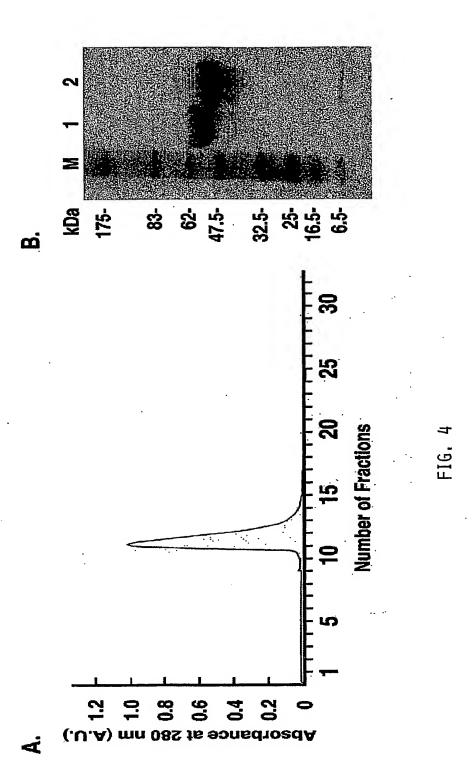
FIG. 2

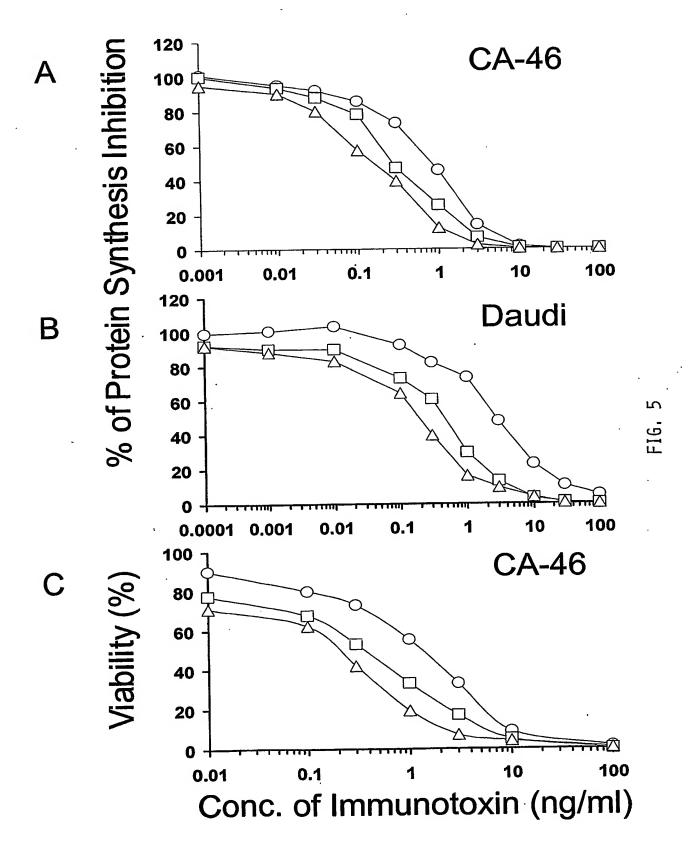
40 cca PRO P 41 gat ASP D

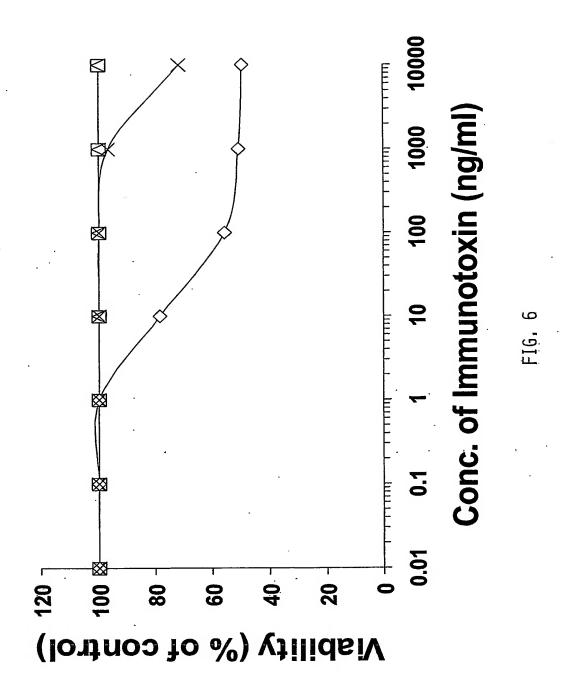
Nucleotide/residue numbering shown first followed by Kabat Numbering

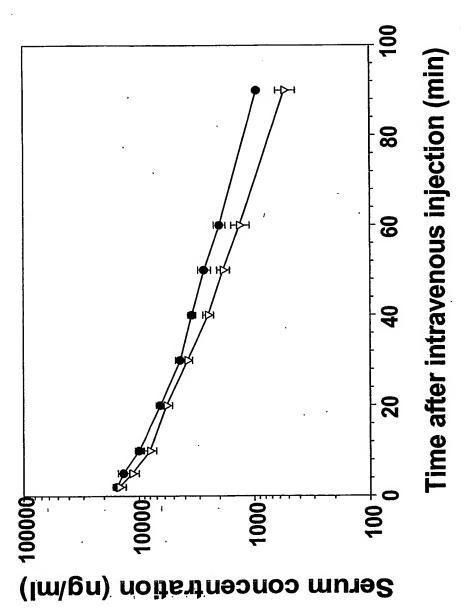
				-	
_	•	49	46 gag GLU B	05	70 has 170 17
1	0	50	47 tgg TRP W	85	79 tac TYR Y
2	1 gaa GLU E	51	48 gtc VAL V	86	80 ctg LEU L
3	2 gtg VAL V	52	49 gca ALA A	87	81 caa GLN Q
4	3 cag GLN Q	53	50 tac TYR Y	88	82 atg MBT N
5	4 ctg LEU L	54,	51 att ILB I	89	82A age SER S
6	5 gtg VAL V	55	52 agt SER S	90	82B agt SER S
7	6 gag GLU E	56	52A agt SER S	91	82C ctg LEU L
8	7 tot SER S	57	52B	92	83 aag LYS K
9	8 ggg GLY G	5 <i>1</i>	52C	93	84 tct SER S
10	9 gga GLY G		53 ggt GLY G	94	85 gag GLU E
11	10 ggc GLY G	59	54 ggt GLY G	95	86 gac ASP D
12	11 tta LEU L	60	st ggt dir c	96	87 aca THR T
13	12 gtg VAL V	61	55 ggt GLY G	97	88 gcc ALA A
14	13 aag LYS K	62	56 acc THR T	98	89 atg MET M
15	14 cct PRO P	63	57 acc THR T	, 99	90 tat TYR Y
16	15 gga GLY G	64	58 tac TYR Y	100	
10		65	59 tat TYR Y		92 tgt CYS C
17	16 ggg GLY G	66	60 cca PRO P	101	
18	17 tcc SER S	67	61 gac ASP D	102	
19	18 ctg LEU L	68	62 act THR T	103	94 aga ARG R
20	19 aaa LYS K	69	63 gtg VAL V	104	95 cat HIS H
21	20 ctc LEU L	70	64 aag LYS K	105	96 agt SER S
22	21 tcc SER S	71	65 ggc GLY G	106	97 ggc GLY G
23	22 tgt CYS C	72	66 cga ARG R	107	98 tac TYR Y
24	23 gca ALA A	73	67 ttc PHE F	108	99 ggt GLY G
25 25	24 gcc ALA A	74	68 acc THR T	109	100 agt SER S
	25 tct SER S	75	69 atc ILE I	110	100A agc SER S
26 27	26 gga GLY G	76	70 tcc SER S	111	100B tac TYR Y
27	27 ttc PHE F	77	71 aga ARG R	112	100C ggg GLY G
28	28 gct ALA A	78	72 gac ASP D	113	100D gtt VAL V
29	29 ttc PHE F	79	73 aat ASN N	114	100E ttg LEU L
30	29 CCC PMS I	80	74 gcc ALA A	115	100F
31	30 agt SER S	81	75 aag LYS K	116	100G
32	31 atc ILE I	82		117	100H
33	32 tat TYR Y	83		118	100I
34	33 gac ASP D	84	78 ctg LEU L	119	100Ј
35	34 atg MET M	04	10 00g 220 2	120	100K ttt PHE P
36	35 tot SER S			121	101 gct ALA A
37	35A			122	102 tac TYR Y
38	35B			123	103 tgg TRP W
39	36 tgg TRP W		•	124	104 ggc GLY G
40	37 gtt VAL V			125	105 caa GLN Q
41	38 cgc ARG R			126	106 ggg GLY G
42	39 cag GLN Q			127	107 act THR T
43	40 act THR T			128	108 ctg LEU L
44	41 ccg PRO P			129	109 gtc VAL V
45	42 gag GLU E			130	110 act THR T
46	43 aag LYS K			131	111 gtc VAL V
47	44 agg ARG R			132	112 tet SER S
48	45 ctg LEU L			133	
	-			133	III YOU MIN N

FIG. 3









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